

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 9, 2002, 00:09:28 ; Search time 8498.8 seconds  
(without alignments)  
31.610 Million cell updates/sec

Title: US-09-851-670-17

Perfect score: 25

Sequence: 1 ctccacttggaatcgcgtacaca 25

Scoring table:

IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 537289281 residues

Total number of hits satisfying chosen parameters: 111874

Minimum DB seq length: 0  
Maximum DB seq length: 60

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*  
1: em\_estfun:\*  
2: em\_estlin:\*  
3: em\_estlin:\*  
4: em\_estlin:\*  
5: em\_estlin:\*  
6: em\_estlin:\*  
7: em\_estlin:\*  
8: em\_estlin:\*  
9: em\_estlin:\*  
10: gb\_est1:\*  
11: gb\_est2:\*  
12: gb\_est2:\*  
13: gb\_gss:\*  
14: em\_gss\_fun:\*  
15: em\_gss\_hum:\*  
16: em\_gss\_inv:\*  
17: em\_gss\_pln:\*  
18: em\_gss\_pro:\*  
19: em\_gss\_rnd:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_other:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description        |
|------------|-------|-------------|--------|-------|--------------------|
| 1          | 14.6  | 58.4        | 49     | 13    | ACH303694 Plasmid  |
| 2          | 14.2  | 56.8        | 27     | 13    | A2663277 IM0542015 |
| 3          | 14    | 56.0        | 27     | 13    | A2477331 IM0296614 |
| 4          | 13.8  | 55.2        | 53     | 10    | AA833683 a37c11.s  |
| 5          | 13.8  | 55.2        | 43     | 10    | AI020738 ub01h04.r |
| 6          | 13.8  | 55.2        | 53     | 13    | TA129A090          |
| 7          | 13.6  | 54.4        | 52     | 11    | BF631900           |
| 8          | 13.4  | 53.6        | 52     | 10    | AA394031           |
| 9          | 13.4  | 53.6        | 60     | 11    | D43017             |
| 10         | 13    | 52.0        | 50     | 10    | AU107342           |
| 11         | 13    | 52.0        | 54     | 10    | AA194224           |
| 12         | 12.8  | 51.2        | 41     | 11    | D25852             |

|      |      |      |    |    |          |                    |
|------|------|------|----|----|----------|--------------------|
| c 13 | 12.6 | 50.4 | 46 | 11 | T73147   | T73147 YC67602..s1 |
| c 14 | 12.6 | 50.4 | 47 | 11 | R52627   | R52627 YG82C02..s1 |
| c 15 | 12.6 | 50.4 | 55 | 10 | AA038583 | AA038583 m185d11.r |
| c 16 | 12.4 | 49.6 | 34 | 13 | A2587290 | A2587290 IM0394420 |
| c 17 | 12.4 | 49.6 | 41 | 10 | AA683660 | AA683660 v103d08.r |
| c 18 | 12.4 | 49.6 | 49 | 10 | AA933986 | AA933986 on95f08.s |
| c 19 | 12.4 | 49.6 | 52 | 10 | AA702879 | AA702879 z180h09.s |
| c 20 | 12.4 | 49.6 | 52 | 10 | AA184887 | AA184887 m146h03.r |
| c 21 | 12.4 | 49.6 | 53 | 10 | AA654368 | AA654368 n162a04.s |
| c 22 | 12.4 | 49.6 | 53 | 10 | AA431961 | AA431961 zw77a05.s |
| c 23 | 12.4 | 49.6 | 53 | 10 | AA484556 | AA484556 n109h06.s |
| c 24 | 12.4 | 49.6 | 53 | 10 | AA542866 | AA542866 n179g03.s |
| c 25 | 12.4 | 49.6 | 53 | 10 | AA557718 | AA557718 n147b09.s |
| c 26 | 12.4 | 49.6 | 53 | 10 | AA568432 | AA568432 n161f08.s |
| c 27 | 12.4 | 49.6 | 53 | 10 | AA583175 | AA583175 nm37d08.s |
| c 28 | 12.4 | 49.6 | 53 | 10 | AA625891 | AA625891 zu87a06.s |
| c 29 | 12.4 | 49.6 | 53 | 13 | A2576214 | A2576214 AST-T013S |
| c 30 | 12.2 | 48.0 | 59 | 13 | A2848297 | A2848297 2M0149K10 |
| c 31 | 12   | 48.0 | 47 | 13 | A2657746 | A2657746 IM0534F09 |
| c 32 | 12   | 48.0 | 50 | 13 | TA19A060 | TA19A060 T. brucei |
| c 33 | 11.8 | 47.2 | 39 | 13 | A2784783 | A2784783 2M0028E02 |
| c 34 | 11.8 | 47.2 | 43 | 10 | AA906764 | AA906764 o116a09.s |
| c 35 | 11.8 | 47.2 | 43 | 13 | A2591374 | A2591374 IM0401M24 |
| c 36 | 11.8 | 47.2 | 45 | 13 | A2761741 | A2761741 IM0556A14 |
| c 37 | 11.8 | 47.2 | 46 | 10 | AA972734 | AA972734 op06g10.s |
| c 38 | 11.8 | 47.2 | 47 | 10 | AA857783 | AA857783 ce42e03.s |
| c 39 | 11.8 | 47.2 | 49 | 13 | CNS074TU | AA429245 clone BA0 |
| c 40 | 11.8 | 47.2 | 50 | 10 | AU102680 | AU102680 A102680   |
| c 41 | 11.8 | 47.2 | 52 | 10 | AA565659 | AA565659 nk26h02.s |
| c 42 | 11.8 | 47.2 | 52 | 11 | BF634385 | BF634385 NF087D01D |
| c 43 | 11.8 | 47.2 | 53 | 10 | A1027736 | A1027736 cv93f05.x |
| c 44 | 11.8 | 47.2 | 54 | 10 | AA630207 | AA630207 ab99g07.s |
| c 45 | 11.8 | 47.2 | 54 | 13 | A2818750 | A2818750 2M0088022 |

#### ALIGNMENTS

|                      |  |       |     |     |             |
|----------------------|--|-------|-----|-----|-------------|
| RESULT 1             | ACH303694  | 49 bp | DNA | GSS | 03-APR-2001 |
| LOCUS                | ACH303694  |       |     |     |             |
| DEFINITION           | Plasmidium chabaudi genome survey sequence, clone PC9H11.plt.      |       |     |     |             |
| DESCRIPTION          | genomic survey sequence.   |       |     |     |             |
| ACCESSION            | AJ303694   |       |     |     |             |
| VERSION              | AJ303694.1 GI:11140201   |       |     |     |             |
| KEYWORDS             | GSS: genome survey sequence.                                       |       |     |     |             |
| SOURCE               | Plasmidium chabaudi.   |       |     |     |             |
| ORGANISM             | Plasmidium chabaudi  |       |     |     |             |
| REFERENCE            | Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmidium.       |       |     |     |             |
| AUTHORS              | 1 (bases 1 to 49)  |       |     |     |             |
| TITLE                | Janssen, C.S., Barrett, M.P., Lawson, D., Quail, M.A., Harris, D., |       |     |     |             |
| JOURNAL              | Bowman, S., Phillips, R.S., and Turner, C.M.                       |       |     |     |             |
| MEDLINE              | Gene discovery in Plasmidium chabaudi by genome survey sequencing  |       |     |     |             |
| REFERENCE            | Mol. Biochem. Parasitol. 113 (2), 251-260 (2001)                   |       |     |     |             |
| AUTHORS              | 2 (bases 1 to 49)  |       |     |     |             |
| TITLE                | Janssen, C.S.  |       |     |     |             |
| JOURNAL              | Direct Submission  |       |     |     |             |
| COMMENT              | Submitted (06-NOV-2000) Division of Infection & Immunity,          |       |     |     |             |
| FEATURES             | University of Glasgow, Joseph Black Building, Glasgow G12 8QQ, UK  |       |     |     |             |
| source               | bases 122 to 170 (OL to OR).                                       |       |     |     |             |
| location/qualifiers  | 1..49  |       |     |     |             |
| ORGANISM             | /organism="Plasmidium chabaudi"                                    |       |     |     |             |
| db_xref="taxon:5825" | /db_xref="taxon:5825"  |       |     |     |             |
| clone="PC9H11.plt"   | /clone="PC9H11.plt"  |       |     |     |             |
| BASE COUNT           | 9 a 11 c 10 g 19 t   |       |     |     |             |
| ORIGIN               |  |       |     |     |             |

Query Match 58.4% Score 14.6; DB 13; Length 49;  
Best Local Similarity 81.0% Pred. No. 1.1e+04;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

| RESULT     | 2   | 48 | 28 |
|------------|---|----|----|
| LOCUS      | AZ663277/c  |    |    |
| DEFINITION | 1M0542015r Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0542015 R, DNA sequence.  |    |    |
| ACCESSION  | AZ663277  |    |    |
| VERSION    | AZ663277.1  |    |    |
| KEYWORDS   | GSS.  |    |    |
| SOURCE     | house mouse.  |    |    |
| ORGANISM   | Mus musculus  |    |    |
| REFERENCE  | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.  |    |    |
| AUTHORS    | 1 (bases 1 to 39)<br>Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamll,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingley,A., von Niederhausern,A. and Wright,D., Weiss,R.<br>Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts<br>Unpublished (2000)<br>Contact: Robert B. Weiss<br>University of Utah<br>Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA<br>Tel: 801 585 5606<br>Fax: 801 585 7177<br>Email: ddunne@genetics.utah.edu<br>Insert Length: 10000 Std Error: 0.00<br>Plate: 0542 row: 0 column: 15<br>Seq primer: CACACAGAAACACCTATGACC<br>Class: plasmid ends<br>High quality sequence stop: 39.   |    |    |
| JOURNAL    | Unpublished (2000)  |    |    |
| COMMENT    | Contact: Robert B. Weiss<br>University of Utah<br>Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA<br>Tel: 801 585 5606<br>Fax: 801 585 7177<br>Email: ddunne@genetics.utah.edu<br>Insert Length: 10000 Std Error: 0.00<br>Plate: 0542 row: 0 column: 15<br>Seq primer: CACACAGAAACACCTATGACC<br>Class: plasmid ends<br>High quality sequence stop: 39.  |    |    |
| FEATURES   | Location/Qualifiers<br>1..39<br>/organism="Mus musculus"<br>/strain="C57Bl/6J"<br>/db_xref="taxon:10090"<br>/clone="UUGC1M0542015"<br>/clone_lib="mouse 10kb plasmid UUGC1M library"<br>/sex="Male"<br>/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"<br>/note="Vector: PWD42nrv; Purified genomic DNA from M. musculus C57Bl/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g114732114[gb AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance." |    |    |
| BASE COUNT | 5 a 7 c 7 g 20 t  |    |    |
| ORIGIN     |   |    |    |

|                       |        |                    |        |            |
|-----------------------|--------|--------------------|--------|------------|
| Query Match           | 56.88; | Score 14.2;        | DB 13; | Length 39; |
| Best Local Similarity | 84.28; | Pred. No. 1.6e+04; |        |            |

|    | Matches | 16, Conservative     | 0; Mismatches | 3; Indels | 0; Gaps |
|----|---------|----------------------|---------------|-----------|---------|
| Qy | 5       | aacttggatcacggtaca   | 23            |           |         |
|    |         |                      |               |           |         |
| Db | 32      | AACTTAATAATCAGGACACA | 14            |           |         |

| RESULT     | 3  |
|------------|--|
| LOCUS      | AZ477331   |
| DEFINITION | AZ477331 27 bp DNA   |
| ACCESSION  | 1M0296G1R Mouse 10kb plasmid UUCCLM library  |
| VERSION    | AZ477331   |
| KEYWORDS   | GI:10635544  |
| SOURCE     | GSS.   |
| ORGANISM   | house mouse.   |
| REFERENCE  | Mus musculus   |
| AUTHORS    | Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi; Mammalia: Eutheria: Rodentia; Scuriognathi; Muridae; Murinae; Mus.   |
|            | 1 (bases 1 to 27)  |
|            | Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  |
| TITLE      | Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts   |
| JOURNAL    | Unpublished (2000)   |
| COMMENT    | Contact: Robert B. Weiss<br>University of Utah Genome Center<br>University of Utah<br>Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT<br>84112 USA<br>Tel.: 801 585 5606<br>Fax: 801 585 7177<br>Email: ddunn@genetics.utah.edu<br>Insert Length: 10000 Std Error: 0.00<br>Plate: 0296 row: G column: 14<br>Seq primer: CACACGAGAAACACCTGTGACC<br>Class: plasmid ends<br>High quality sequence. stop: 27. |

FEATURES  
SOURCE

Location/Qualifiers  
1. .27  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="MUGCIM0296G14"  
/clone\_lib="Mouse 10kb plasmid MUGCIM Library"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMW42 (gii4732114|gb|AF19072.1)', a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

| BASE COUNT<br>ORIGIN | 9 a | 6 c | 5 g | 7 t |
|----------------------|-----|-----|-----|-----|
| Query Match          |     |     |     |     |



[illegible]

```

Email: gdmay@noble.org
Insert Length: 52 Std Error: 0.00
Plate: 016 ROW: F COLUMN: 05
Seq primer: TCACACAGGAACACGTATGCAC.

FEATURES
    source
        1..52
            /organism="Medicago truncatula"
            /db_xref="taxon:3880"
            /clone="NF016F050R"
            /clone_lib="Drought"
            /tissue_type="Plantlets"
            /dev_stage="Pooled timepoints"
            /note="Vector: Lambda ZAP; Contains a mixture of entire
            plantlets harvested in a series of days-post-watering
            timepoints."

BASE COUNT      21 a      17 c      3 g      11 t
ORIGIN

Query Match      54.4%; Score 13.6; DB 11; Length 52;
Best Local Similarity 80.0%; Pred. No. 3.1e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      6 acttgaatcacgcgtacaca 25
        ||||| || || || |||||
        10 ACTTCCAAACAACGTACACAC 29

RESULT 8
AA394031/c
LOCUS
DEFINITION
AA394031 52 bp mRNA EST 16-MAY-1997
zr185ell.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:729164
5' similar to WP:DI022.1 CE02575 UBIQUITIN-CONJUGATING ENZYME ; ,
mRNA sequence.
AA394031
AA394031.1 GI:2047018
EST.

ORGANISM
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 52)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B.,
Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wyile
, T., Waterston, R. and Wilson, R.
Washu-Merck EST Project 1997
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone; similarity on wrong strand
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1..52
/organism="Homo sapiens"
/db_xref="GDB:5925693"
/db_xref="taxon:9606"
/clone="IMAGE:729164"
/clone_lib="Soares_testis_NHT"
/sex="male"
/lab_host="DH10B"
/note="Vector: pUT7AD-Pac (Pharmacia) with a modified
polylinker. Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech Laboratories
, Inc., and primed with a Not I - oligo(dT) primer [5'

```



/clone="IMAGE:628710"  
/clone\_lib="Stratagene muscle 937209"  
/issue\_type="muscle"  
/dev\_stage="adult"  
/lab\_host="SOLR (kanamycin resistant)"  
/note="Organ: skeletal muscle; Vector: pBluescript SK-;  
Site\_1: EcoRI; Site\_2: XhoI; Cloned unidirectionally.  
Primer: Oligo dT. Skeletal muscle from patient with  
malignant hyperthermia. Average insert size: 1.0 kb;  
Uni-ZAP XR Vector: -5' adaptor sequence: 5' GAATTCGCGCAGCAG  
3' -3' adaptor sequence: 5' CTCGAGTTTCTTTTCTTTT 3'"

BASE COUNT  
14 a 9 c 9 g 21 t 1 others

ORIGIN

Query Match  
Best Local Similarity 72.7%; Score 13; DB 10; Length 54;  
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 2 tcccaactggaatcacggtaca 23  
18 tcccaactggaatcacggtaca 39

RESULT 12  
D25852 41 bp mRNA EST 30-NOV-1995  
LOCUS HUMS04228 Human colon mucosa Homo sapiens cDNA clone cm2172.3',  
DEFINITION mRNA sequence.  
ACCESSION D25852  
VERSION D25852.1 GI:500520  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE 1 (bases 1 to 41)  
Okubo, K., Yoshii, J., Yokouchi, H., Kameyama, M. and Matsubara, K.  
Global analysis of gene expression in colon mucosa: a large scale  
random cDNA sequencing analysis  
JOURNAL Unpublished (1994)  
COMMENT Contact: Okubo, K., Itoh, K., Yoshii, J., Yokouchi, H. and Matsubara, K.  
Institute for Molecular and Cellular Biology  
Osaka University  
3-1 Yamada-oka, Suita, Osaka 565, Japan.  
FEATURES  
source  
1.41  
Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="cm2172"  
/clone\_lib="Human colon mucosa"  
/note="Adult male, tissue type = colon mucosa"

BASE COUNT  
15 a 8 c 3 g 15 t

ORIGIN

Query Match  
Best Local Similarity 51.2%; Score 12.8; DB 11; Length 41;  
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 ctccaactggaatcacggtaca 24  
4 ctccaactggaatcacggtaca 27

RESULT 13  
T73147 46 bp mRNA EST 02-MAR-1995  
LOCUS T73147/c  
DEFINITION yc67e02.s1 Stratagene liver (#937224) Homo sapiens cDNA clone  
IMAGE:85754.3' similar to gb:xs4486\_mnal PLASMA PROTEASE C1  
INHIBITOR PRECURSOR (HUMAN);, mRNA sequence.  
ACCESSION T73147  
VERSION T73147.1 GI:689822

KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE 1 (bases 1 to 46)  
Hallier, L., Lennow, G., Becker, M., Bonaldo, M.F., Chappel, B.,  
Chisoe, S., Dietrich, N., Dubuque, T., Favell, A., Gish, W., Hawkins,  
B., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, M., Maris, E., Moore  
B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,  
Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, D., Trevisan, E.,  
Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Maria, M.  
Generation and analysis of 280,000 human expressed sequence tags  
Genome Res. 6 (9), 807-828 (1996)  
97044478  
TITLE  
JOURNAL  
MEDLINE  
COMMENT  
Contact: Wilson, R.K.  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.edu  
Insert Size: 1353  
High quality sequence starts: 1 High quality sequence stops: 1  
Source: IMAGE Consortium, LNL This clone is available royalty-free  
through LNL; contact the IMAGE Consortium (info@image.lnl.gov)  
for further information. Trace considered overall poor quality  
Insert length: 1353 Std Error: 0.00  
Seq primer: -21m13  
High quality sequence stop: 1.  
FEATURES  
source  
1.46  
Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="GDB:502811"  
/db\_xref="taxon:9606"  
/clone="IMAGE:85754"  
/clone\_lib="Stratagene liver (#937224)"  
/sex="male"  
/dev\_stage="49 years old"  
/lab\_host="SOLR cells (kanamycin resistant)"  
/note="Organ: liver; Vector: pBluescript SK; Site\_1: EcoRI  
; Site\_2: XhoI; Cloned unidirectionally. Primer: Oligo  
dT. Hepatectomy from normal male caucasian. Average insert  
size: 1.1 kb; Uni-ZAP XR Vector: -5' adaptor sequence: 5'  
GAATTCGCGCAGCAG 3' -3' adaptor sequence: 5'  
CTCGAGTTTCTTTTCTTTT 3'"

BASE COUNT  
15 a 12 c 11 g 7 t 1 others

ORIGIN

Query Match  
Best Local Similarity 50.4%; Score 12.6; DB 11; Length 46;  
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 ctccaactggaatcacggt 20  
28 ctccaactggaatcacggt 9

RESULT 14  
R52627 47 bp mRNA EST 18-MAY-1995  
LOCUS R52627  
DEFINITION yg82c02.s1 Soares infant brain INIB Homo sapiens cDNA clone  
IMAGE:39999.3' similar to gb:U137101HUMSCALDH Human scRNA molecule,  
transcribed from Aliu (rRNA); gb:M62424 THROMBIN RECEPTOR PRECURSOR  
(HUMAN);, mRNA sequence.  
ACCESSION R52627  
VERSION R52627.1 GI:814529  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE 1 (bases 1 to 47)

**AUTHORS**  
 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Treweek, E., Waterston, R., Williamson, A., Woldmann, P. and Wilson, R.  
**TITLE**  
 The WashU-Merck EST Project  
**JOURNAL**  
 Unpublished (1995)  
**COMMENT**  
 Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@wustl.edu  
 Insert Size: 1970  
 High quality sequence starts: 1 High quality sequence stops: 1  
 Source: IMAGE Consortium, LNL This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information. Trace considered overall poor quality  
 Insert Length: 1970 Std Error: 0.00  
 Seq primer: Promega -21m13  
 High quality sequence stop: 1.  
 Location/Qualifiers

# FEATURES

source  
 1..47  
 /organism="Homo sapiens"  
 /db\_xref="GDB:412540"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:39999"  
 /clone\_lib="Soares infant brain INTB"  
 /sex="female"  
 /dev\_stage="73 days post natal"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /note="Organ: whole brain; Vector: Lnfmid BA; Site: 1: Not I; Site: 2: Hind III; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', AACTGGAAGATTCGCGCGCCGACGAGATTTTGTGTGTGT 3']; double-stranded cDNA was ligated to Hind III adaptors (Pharmacia), digested with Not I and directionally cloned into the Not I and Hind III sites of the Lnfmid BA vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."

# BASE COUNT

7 a 10 c 17 g 10 t 3 others

**Query Match**  
 Best Local Similarity 50.4%; Score 12.6; DB 11; Length 47;  
 Matches 15; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 ctccacttggaatcacggtta 21  
 ||| | ||||| |||||  
 Db 9 CTCANCGNTGTATATCCCGTA 29

**RESULT** 15  
 AA038583 55 bp mRNA EST 28-AUG-1996  
 LOCUS m185d11.r1 Soares mouse p3NMFI9.5 Mus musculus cDNA clone  
 DEFINITION IMAGE:473397 5' similar to SW:KTH\_HUMAN P23919 THYMIDYLATE KINASE  
 ; mRNA sequence.  
 AA038583  
 EST.  
 AA038583.1 GI:1513989  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
**REFERENCE**  
 1 (bases 1 to 55)  
 Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisler, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.  
**TITLE**  
 The WashU-HMI Mouse EST Project  
**JOURNAL**  
 Unpublished (1996)

# COMMENT

Contact: Marra M/Mouse EST Project  
 WashU-HMI Mouse EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@wustl.edu  
 This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.  
 MGI:284141  
 Trace considered overall poor quality  
 Possible reversed clone; similarity on wrong strand  
 Seq primer: -28m13 rev2 from Amersham  
 High quality sequence stop: 1.  
 Location/Qualifiers

# FEATURES

source

1..55  
 /organism="Mus musculus"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:473397"  
 /clone\_lib="Soares mouse p3NMFI9.5"  
 /dev\_stage="19.5 dpc total fetus"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /note="Vector: pT73D (Pharmacia) with a modified polylinker; Site: 1: Not I; Site: 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TCTTACCAATCGAAGTGGAGCGCGCGCATTTTGTGTGTGT 3']; double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA was kindly provided by Dr. Minoru Ko (Wayne State University)."

# BASE COUNT

9 a 13 c 23 g 10 t

**Query Match**  
 Best Local Similarity 50.4%; Score 12.6; DB 10; Length 55;  
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 7 ctggaatcacggtacaca 25  
 |||| | ||||| |||||  
 Db 43 CTGCGACGACGCGTCCACA 25

Search completed: March 9, 2002, 00:09:30  
 Job time: 11046 sec

**THIS PAGE BLANK (USPTO)**

---